SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT:

        Goodearl, Andrew
        Stroobant, Paul
        Minghetti, Luisa
        Waterfield, Michael
        Marchionni, Mark
        Chen, Mario
        Hiles, Ian

    (ii) TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR PREPARATION AND USE

    (iii) NUMBER OF SEQUENCES: 189

    (iv) CORRESPONDENCE ADDRESS:

        (A) ADDRESSEE: Clark & Elbing LLP
        (B) STREET: 176 Federal Street
        (C) CITY: Boston
        (D) STATE: Massachusetts
        (E) COUNTRY: U.S.A.
        (F) ZIP: 02110

    (v) COMPUTER READABLE FORM:

        (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
        (B) COMPUTER: IBM Compatible Pentium
        (C) OPERATING SYSTEM: Windows95
        (D) SOFTWARE: FastSeq Version 2.0

    (vi) CURRENT APPLICATION DATA:

        (A) APPLICATION NUMBER: 08/736,019
        (B) FILING DATE: 22-OCT-1996
        (C) CLASSIFICATION:

    (vii) PRIOR APPLICATION DATA:

        (A) APPLICATION NUMBER: 08/471,833
        (B) FILING DATE: 06-JUN-1995

    (vii) PRIOR APPLICATION DATA:

        (A) APPLICATION NUMBER: 08/036,555
        (B) FILING DATE: 24-MAR-1993

    (vii) PRIOR APPLICATION DATA:

```
            (A) APPLICATION NUMBER: 07/965,173
            (B) FILING DATE:        23-OCT-1992

    (vii) PRIOR APPLICATION DATA:

            (A) APPLICATION NUMBER: 07/907,138
            (B) FILING DATE:        30-JUN-1992

    (vii) PRIOR APPLICATION DATA:

            (A) APPLICATION NUMBER: 07/940,389
            (B) FILING DATE:        03-SEP-1992

    (vii) PRIOR APPLICATION DATA:

            (A) APPLICATION NUMBER: 07/863,703
            (B) FILING DATE:        03-APR-1992

    (vii) PRIOR APPLICATION DATA:

            (A) APPLICATION NUMBER: UK 91 07566.3
            (B) FILING DATE:        10-APR-1991

   (viii) ATTORNEY/AGENT INFORMATION:

            (A) NAME:                 Bieker-Brady, Kristina
            (B) REGISTRATION NUMBER: 39,109
            (C) REFERENCE/DOCKET NUMBER: 04585/00200Q

    (ix) TELECOMMUNICATION INFORMATION:

            (A) TELEPHONE:            (617) 428-0200
            (B) TELEFAX:              (617) 428-7045
            (C) TELEX:

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     1:

    (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH:               8
            (B) TYPE:                 amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY:             linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:


Phe Lys Gly Asp Ala His Thr Glu
 1               5
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 2:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine; Xaa in position 12 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Xaa Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Xaa Lys

1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 3:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 12
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine; Xaa in position 10 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Xaa Thr Glu Thr Ser Ser Ser Gly Leu Xaa Leu Lys
1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 4:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 9
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Xaa Lys Leu Gly Glu Met Trp Ala Glu
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 5:

   (i) SEQUENCE CHARACTERISTICS:

      (A) LENGTH: 7
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear

   (ix) FEATURE:

      (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Xaa Leu Gly Glu Lys Arg Ala
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 6:

   (i) SEQUENCE CHARACTERISTICS:

      (A) LENGTH: 16
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear

   (ix) FEATURE:

      (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Xaa Ile Lys Ser Glu His Ala Gly Leu Ser Ile Gly Asp Thr Ala Lys

 1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 7:

   (i) SEQUENCE CHARACTERISTICS:

      (A) LENGTH: 13

-104-

```
          (B) TYPE:              amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY:          linear

     (ix) FEATURE:

          (D)  OTHER INFORMATION:  Xaa in position 1 is Lysine or Arginine.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Xaa Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys

 1              5                  10


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    8:

     (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH:            16
          (B) TYPE:              amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY:          linear

     (ix) FEATURE:

          (D)  OTHER INFORMATION:  Xaa in position 1 is Lysine or Arginine.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Xaa Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys
 1              5                  10                 15


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    9:

     (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH:            13
          (B) TYPE:              amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY:          linear

     (ix) FEATURE:

          (D)  OTHER INFORMATION:  Xaa in position 1 is Lysine or
Arginine and Xaa in position 12 is unknown.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Xaa Met Ser Glu Tyr Ala Phe Phe Val Gln Thr Xaa Arg
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Xaa Ser Glu His Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys

1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine; Xaa in position 8 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Xaa Ala Gly Tyr Phe Ala Glu Xaa Ala Arg

1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9

(B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

     (ix) FEATURE:

          (D) OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine; Xaa in position 7 is unknown.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Xaa Lys Leu Glu Phe Leu Xaa Ala Lys
  1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 13:

     (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 11
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

     (ix) FEATURE:

          (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Xaa Thr Thr Glu Met Ala Ser Glu Gln Gly Ala

  1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 14:

     (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 10
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

     (ix) FEATURE:

          (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Xaa Ala Lys Glu Ala Leu Ala Ala Leu Lys

1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 15:

    (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 8
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear

    (ix) FEATURE:

            (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Xaa Phe Val Leu Gln Ala Lys Lys
    1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 16:

    (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 6
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear

    (ix) FEATURE:

            (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Xaa Leu Gly Glu Met Trp
    1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 17:

    (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 16
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Glu Tyr Lys Cys Leu Lys Phe Lys Trp Phe Lys Lys Ala Thr Val Met
1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 18:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 10
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 8 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Glu Ala Lys Tyr Phe Ser Lys Xaa Asp Ala
1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 19:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 7
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 2 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Glu Xaa Lys Phe Tyr Val Pro
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 20:

    (i) SEQUENCE CHARACTERISTICS:

```
        (A)  LENGTH:              26
        (B)  TYPE:                amino acid
        (C)  STRANDEDNESS:
        (D)  TOPOLOGY:            linear

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Glu Leu Ser Phe Ala Ser Val Arg Leu Pro Gly Cys Pro Pro Gly Val
 1               5                  10                  15

Asp Pro Met Val Ser Phe Pro Val Ala Leu
             20                  25


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     21:

    (i)  SEQUENCE CHARACTERISTICS:

        (A)  LENGTH:              2003
        (B)  TYPE:                nucleic acid
        (C)  STRANDEDNESS:        single
        (D)  TOPOLOGY:            linear


    (ix)  FEATURE:

        (D)  OTHER INFORMATION:  N in positions 31 and 32 could be
either A or G.

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GGAATTCCTT TTTTTTTTTT TTTTTTTCTT NNTTTTTTTT TGCCCTTATA CCTCTTCGCC   60

TTTCTGTGGT TCCATCCACT TCTTCCCCCT CCTCCTCCCA TAAACAACTC TCCTACCCCT  120

GCACCCCCAA TAAATAAATA AAAGGAGGAG GGCAAGGGGG GAGGAGGAGG AGTGGTGCTG  180

CGAGGGGAAG GAAAAGGGAG GCAGCGCGAG AAGAGCCGGG CAGAGTCCGA ACCGACAGCC  240

AGAAGCCCGC ACGCACCTCG CACC ATG AGA TGG CGA CGC GCC CCG CGC CGC    291
                           Met Arg Trp Arg Arg Ala Pro Arg Arg
                            1               5

TCC GGG CGT CCC GGC CCC CGG GCC CAG CGC CCC GGC TCC GCC GCC CGC    339
Ser Gly Arg Pro Gly Pro Arg Ala Gln Arg Pro Gly Ser Ala Ala Arg
 10               15                  20                  25

TCG TCG CCG CCG CTG CCG CTG CTG CCA CTA CTG CTG CTG CTG GGG ACC    387
Ser Ser Pro Pro Leu Pro Leu Leu Pro Leu Leu Leu Leu Leu Gly Thr
                 30                  35                  40

GCG GCC CTG GCG CCG GGG GCG GCG GCC GGC AAC GAG GCG GCT CCC GCG    435
```

-110-

```
Ala Ala Leu Ala Pro Gly Ala Ala Ala Gly Asn Glu Ala Ala Pro Ala
            45              50              55

GGG GCC TCG GTG TGC TAC TCG TCC CCG CCC AGC GTG GGA TCG GTG CAG          483
Gly Ala Ser Val Cys Tyr Ser Ser Pro Pro Ser Val Gly Ser Val Gln
            60              65              70

GAG CTA GCT CAG CGC GCC GCG GTG GTC ATC GAG GGA AAG GTG CAC CCG          531
Glu Leu Ala Gln Arg Ala Ala Val Val Ile Glu Gly Lys Val His Pro
    75              80              85

CAG CGG CGG CAG CAG GGG GCA CTC GAC AGG AAG GCG GCG GCG GCG GCG          579
Gln Arg Arg Gln Gln Gly Ala Leu Asp Arg Lys Ala Ala Ala Ala Ala
    90              95              100             105

GGC GAG GCA GGG GCG TGG GGC GGC GAT CGC GAG CCG CCA GCC GCG GGC          627
Gly Glu Ala Gly Ala Trp Gly Gly Asp Arg Glu Pro Pro Ala Ala Gly
                110             115             120


CCA CGG GCG CTG GGG CCG CCC GCC GAG GAG CCG CTG CTC GCC GCC AAC          675
Pro Arg Ala Leu Gly Pro Pro Ala Glu Glu Pro Leu Leu Ala Ala Asn
            125             130             135

GGG ACC GTG CCC TCT TGG CCC ACC GCC CCG GTG CCC AGC GCC GGC GAG          723
Gly Thr Val Pro Ser Trp Pro Thr Ala Pro Val Pro Ser Ala Gly Glu
            140             145             150

CCC GGG GAG GAG GCG CCC TAT CTG GTG AAG GTG CAC CAG GTG TGG GCG          771
Pro Gly Glu Glu Ala Pro Tyr Leu Val Lys Val His Gln Val Trp Ala
    155             160             165

GTG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG CTC ACC GTG CGC CTG          819
Val Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu Leu Thr Val Arg Leu
170             175             180             185

GGG ACC TGG GGC CAC CCC GCC TTC CCC TCC TGC GGG AGG CTC AAG GAG          867
Gly Thr Trp Gly His Pro Ala Phe Pro Ser Cys Gly Arg Leu Lys Glu
            190             195             200

GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAC GCC AAC AGC ACC AGC          915
Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Asp Ala Asn Ser Thr Ser
            205             210             215

CGC GCG CCG GCC GCC TTC CGA GCC TCT TTC CCC CCT CTG GAG ACG GGC          963
Arg Ala Pro Ala Ala Phe Arg Ala Ser Phe Pro Pro Leu Glu Thr Gly
            220             225             230

CGG AAC CTC AAG AAG GAG GTC AGC CGG GTG CTG TGC AAG CGG TGC GCC          1011
Arg Asn Leu Lys Lys Glu Val Ser Arg Val Leu Cys Lys Arg Cys Ala
    235             240             245
```

-111-

```
TTG CCT CCC CAA TTG AAA GAG ATG AAA AGC CAG GAA TCG GCT GCA GGT    1059
Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala Gly
250             255             260             265

TCC AAA CTA GTC CTT CGG TGT GAA ACC AGT TCT GAA TAC TCC TCT CTC    1107
Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu
            270             175             180

AGA TTC AAG TGG TTC AAG AAT GGG AAT GAA TTG AAT CGA AAA AAC AAA    1155
Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys
            185             190             195

CCA CAA AAT ATC AAG ATA CAA AAA AAG CCA GGG AAG TCA GAA CTT CGC    1203
Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg

        200             205             210

ATT AAC AAA GCA TCA CTG GCT GAT TCT GGA GAG TAT ATG TGC AAA GTG    1251
Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val
    215             220             225

ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT GCC AAT ATC ACC ATC GTG    1299
Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val
230             235             240             245

GAA TCA AAC GCT ACA TCT ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA    1347
Glu Ser Asn Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val
            250             255             260

AAA TGT GCG GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC    1395
Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
            265             270             275

TTC ATG GTG AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG TGC AAG TGC    1443
Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
            280             285             290

CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC    1491
Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser
            295             300             305

TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA    1530
Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
400             405             410

TAGGAGCATG CTCAGTTGGT GCTGCTTTCT TGTTGCTGCA TCTCCCCTCA GATTCCACCT    1590

AGAGCTAGAT GTGTCTTACC AGATCTAATA TTGACTGCCT CTGCCTGTCG CATGAGAACA    1650

TTAACAAAAG CAATTGTATT ACTTCCTCTG TTCGCGACTA GTTGGCTCTG AGATACTAAT    1710
```

AGGTGTGTGA GGCTCCGGAT GTTTCTGGAA TTGATATTGA ATGATGTGAT ACAAATTGAT 1770

AGTCAATATC AAGCAGTGAA ATATGATAAT AAAGGCATTT CAAAGTCTCA CTTTTATTGA 1830

TAAAATAAAA ATCATTCTAC TGAACAGTCC ATCTTCTTTA TACAATGACC ACATCCTGAA 1890

AAGGGTGTTG CTAAGCTGTA ACCGATATGC ACTTGAAATG ATGGTAAGTT AATTTTGATT 1950

CAGAATGTGT TATTTGTCAC AAATAAACAT AATAAAAGGA AAAAAAAAAA AAA   2003

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 22:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 12
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 11 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Xaa Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 23:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 11
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 9 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Thr Glu Thr Ser Ser Ser Gly Leu Xaa Leu Lys

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 24:

   (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 12
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: -   linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys

 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 25:

   (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 9
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

   (ix) FEATURE:

        (D)   OTHER INFORMATION: Xaa in position 7 is unknown.

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Ala Gly Tyr Phe Ala Glu Xaa Ala Arg
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 26:

   (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 10
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Thr Thr Glu Met Ala Ser Glu Gln Gly Ala

1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 27:

    (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 9
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Ala Lys Glu Ala Leu Ala Ala Leu Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 28:

    (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 7
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Phe Val Leu Gln Ala Lys Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 29:

    (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 21
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Glu Thr Gln Pro Asp Pro Gly Gln Ile Leu Lys Lys Val Pro Met Val
 1   5   10   15

Ile Gly Ala Tyr Thr
            20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 30:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 21
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in positions 1, 3, 17 and 19 is
unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Xaa Glu Xaa Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys Glu
 1   5   10   15

Xaa Gly Xaa Gly Lys
        20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 31:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 32:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 8
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 6 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Lys Leu Glu Phe Leu Xaa Ala Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 33:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 9
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Xaa Val His Gln Val Trp Ala Ala Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 34:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 14
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or
Argininel; Xaa in position 11 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Xaa Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly

 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 35:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 14
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine; Xaa in position 13 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Xaa Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr

 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 36:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 9
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Xaa Trp Phe Val Val Ile Glu Gly Lys
  1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 37:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 16
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

(ix) FEATURE:

       (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Xaa Ala Ser Pro Val Ser Val Gly Ser Val Gln Glu Leu Val Gln Arg
 1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 38:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

       (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Xaa Val Cys Leu Leu Thr Val Ala Ala Leu Pro Pro Thr
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 39:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 7
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

       (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine; Xaa in position 6 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Xaa Asp Leu Leu Leu Xaa Val
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 40:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 39
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```
Cys Thr Cys Gly Cys Cys Lys Cys Cys Arg Thr Thr Cys Ala Cys Arg
 1           5               10              15

Cys Ala Gly Ala Ala Gly Gly Thr Cys Thr Thr Cys Thr Cys Cys Thr
            20              25              30

Thr Cys Thr Cys Ala Gly Cys
        35
```


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 41:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 24
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```
Cys Cys Thr Cys Gly Cys Thr Cys Cys Thr Thr Cys Thr Thr Cys Thr
 1           5               10              15

Thr Gly Cys Cys Cys Thr Thr Cys
            20
```


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 42:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 60
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

AAGTGCCCAA ATGAGTTTAC TGGTGATCGC TGCCAAAACT ACGTAATGGC CAGCTTCTAC   60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 43:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 36
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AGTACGTCCA CTCCCTTTCT GTCTCTGCCT GAATAG   36

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 44:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 569
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

AAGGCGGAGG AGCTGTACCA GAAGAGAGTG CTGACCATAA CCGGCATCTG CATCGCCCTC   60

CTTGTGGTCG GCATCATGTG TGTGGTGGCC TACTGCAAAA CCAAGAAACA GCGGAAAAAG 120

CTGCATGACC GTCTTCGGCA GAGCCTTCGG TCTGAACGAA ACAATATGAT GAACATTGCC 180

AATGGGCCTC ACCATCCTAA CCCACCCCCC GAGAATGTCC AGCTGGTGAA TCAATACGTA 240

TCTAAAAACG TCATCTCCAG TGAGCATATT GTTGAGAGAG AAGCAGAGAC ATCCTTTTCC 300

ACCAGTCACT ATACTTCCAC AGCCCATCAC TCCACTACTG TCACCCAGAC TCCTAGCCAC 360

AGCTGGAGCA ACGGACACAC TGAAAGCATC CTTTCCGAAA GCCACTCTGT AATCGTGATG 420

TCATCCGTAG AAAACAGTAG GCACAGCAGC CCAACTGGGG GCCCAAGAGG ACGTCTTAAT 480

GGCACAGGAG GCCCTCGTGA ATGTAACAGC TTCCTCAGGC ATGCCAGAGA AACCCCTGAT 540

TCCTACCGAG ACTCTCCTCA TAGTGAAAG   569

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 45:

(i) SEQUENCE CHARACTERISTICS:

             (A) LENGTH: 8
             (B) TYPE: amino acid
             (C) STRANDEDNESS:
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Val His Gln Val Trp Ala Ala Lys
  1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 46:

        (i) SEQUENCE CHARACTERISTICS:

             (A) LENGTH: 13
             (B) TYPE: amino acid
             (C) STRANDEDNESS:
             (D) TOPOLOGY: linear

        (ix) FEATURE:

             (D) OTHER INFORMATION: Xaa in position 10 is unknown.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
  1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 47:

        (i) SEQUENCE CHARACTERISTICS:

             (A) LENGTH: 13
             (B) TYPE: amino acid
             (C) STRANDEDNESS:
             (D) TOPOLOGY: linear

        (ix) FEATURE:

             (D) OTHER INFORMATION: Xaa in position 12 is unknown.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
  1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 48:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 8
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Trp Phe Val Val Ile Glu Gly Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 49:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 15
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Ala Ser Pro Val Ser Val Gly Ser Val Gln Glu Leu Val Gln Arg
 1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 50:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 12
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Val Cys Leu Leu Thr Val Ala Ala Leu Pro Pro Thr
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 51:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 9

(B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Lys Val His Gln Val Trp Ala Ala Lys
  1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 52:

      (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 13
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear

      (ix) FEATURE:

            (D)   OTHER INFORMATION: Xaa in position 12 is unknown.

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lys
  1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 53:

      (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 6
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear

      (ix) FEATURE:

            (D)   OTHER INFORMATION: Xaa in position 5 is unknown.

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Asp Leu Leu Leu Xaa Val
  1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 54:

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 20
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ix) FEATURE:

    (D) OTHER INFORMATION: N at positions 3, 12 and 18 is C
or T; N at position 6 is A or G; N at positions 9 and 15 is A, T,
G or C.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

TTNAANGGNG ANGCNCANAC   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 55:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at positions 7 and 13 is C or T;
N at positions 4, 10, and 16 is A or G; N at position 19 is A, T, G
or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CATNTANTCN TANTCNTCNG C   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 56:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at positions 3 and 15 is C or T;

N at positions 6, 9, and 18 is A, T, G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TGNTCNGANG CCATNTCNGT   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 57:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at positions 3 and 14 is C or T;
N at position 6 is A or G; N at positions 9 and 17 is A, T, G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TGNTCNCTNG CCATNTCNGT   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 58:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at position 3 is A, G or T; N
at position 18 is C or T; N at positions 6, 12, and 15 is A, T,
G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CCNATNACCA TNGGNACNTT   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 59:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20

```
                (B)  TYPE:                nucleic acid
                (C)  STRANDEDNESS:         single
                (D)  TOPOLOGY:             linear

        (ix)  FEATURE:

                (D)  OTHER INFORMATION: N at position 12 is C or T; N at
position 15 is A or G; N at positions 3, 9 and 18 is A, T, G or C.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GCNGCCCANA CYTGRTGNAC                                           20


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     60:

        (i) SEQUENCE CHARACTERISTICS:

                (A)  LENGTH:               20
                (B)  TYPE:                 nucleic acid
                (C)  STRANDEDNESS:         single
                (D)  TOPOLOGY:             linear

        (ix)  FEATURE:

                (D)  OTHER INFORMATION:  N at positions 3 and 9 is C or T;
N at positions 5 and 8 is A or G; N at position 6 is A, T, G or C.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GCNTCNGGNT CCATNAANAA                                           20


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     61:

        (i) SEQUENCE CHARACTERISTICS:

                (A)  LENGTH:               20
                (B)  TYPE:                 nucleic acid
                (C)  STRANDEDNESS:         single
                (D)  TOPOLOGY:             linear

        (ix)  FEATURE:

                (D)  OTHER INFORMATION: N at position 6 is A, G or T;  N at
position 3 is C or T; N at position 15 is A or G; N at positions 9
and 11 is A, T, G or C.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CCNTCNATNA CNACNAACCA                                           20
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 62:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 17
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at positions 6 and 9 is A or G;
N at positions 3, 11 and 14 is A, T, G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

TCNGCNAANT ANCCNGC   17

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 63:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at positions 12 and 15 is C or T;
N at positions 3, 6, 9 and 17 is A, T, G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GCNGCNAGNG CNTCNTTNGC   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 64:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at positions 6, 12 and 15 is C or T;
N at positions 3, 9, and 18 is A, T, G or C.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GCNGCNAANG CNTCNTTNGC   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 65:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at positions 3 and 9 is C or T;
N at position 18 is A or G; N at positions 6, 12 and 15 is A, T, G
or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TTNTTNGCNT GNAGNACNAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 66:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at positions 3, 9 and 12 is C or T;
N at position 18 is A or G; N at positions 6 and 15 is A, T, G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

TTNTTNGCNT GNAANACNAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 67:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 17
        (B) TYPE: nucleic acid

```
        (C)  STRANDEDNESS:          single
        (D)  TOPOLOGY:              linear

    (ix)  FEATURE:

        (D)  OTHER INFORMATION:  N at positions 9 and 12 is C or T;
N at positions 3, 6 and 15 is A, T, G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TGNACNAGNT CNTGNAC                                           17


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    68:

    (i) SEQUENCE CHARACTERISTICS:

        (A)  LENGTH:               17
        (B)  TYPE:                 nucleic acid
        (C)  STRANDEDNESS:         single
        (D)  TOPOLOGY:             linear

    (ix)  FEATURE:

        (D)  OTHER INFORMATION: N at positions 6, 9, and 12 is C or
T; N at positions 3 and 15 is A, T, G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

TGNACNAANT CNTGNAC                                           17


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    69:

    (i) SEQUENCE CHARACTERISTICS:

        (A)  LENGTH:               21
        (B)  TYPE:                 nucleic acid
        (C)  STRANDEDNESS:         single
        (D)  TOPOLOGY:             linear

    (ix)  FEATURE:

        (D)  OTHER INFORMATION:  N at position 7 is C or T; N at
positions 4 and 16 is A or G; N at positions 10, 13 and 19 is A,
T, G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CATNTANTCN CCNGANTCNG C                                      21
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 70:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at position 7 is C or T; N at
positions 4, 13 and 16 is A or G; N at positions 10 and 19 is A,
T, G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CATNTANTCN CCNCTNTCNG C   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 71:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at positions 10 and 19 is C or T;
N at position 4 is A or G; N at positions 1, 7, 13 and 16 is A, T,
G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

NGANTCNGCN AANGANGCNT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 72:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

(D) OTHER INFORMATION: N at position 19 is C or T; N at position 4 is A or G; N at positions 1, 7, 10, 13 and 16 is A, T, G or C.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

NGANTCNGCN AGNGANGCNT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 73:

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 21
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: N at positions 10 and 19 is C or T; N at positions 1 and 4 is A or G; N at positions 7, 13 and 16 is A, T, G or C.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

NCTNTCNGCN AANGANGCNT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 74:

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 21
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: N at position 19 is C or T; N at positions 1 and 14 is A or G; N at positions 7, 10, 13 and 16 is A, T, G or C.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

NCTNTCNGCN AGNGANGCNT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 75:

(i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 21
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

        (ix) FEATURE:

                (D) OTHER INFORMATION: N at positions 10 and 19 is C or T;
N at positions 4 and 13 is A or G; N at positions 1, 7 and 16 is
A, T, G or C.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

NGANTCNGCN AANCTNGCNT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 76:

        (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 21
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

        (ix) FEATURE:

                (D) OTHER INFORMATION: N at position 19 is C or T; N at
positions 4 and 13 is A or G; N at positions 1, 7, 10 and 16 is
A, T, G or C.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

NGANTCNGCN AGNCTNGCNT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 77:

        (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 730
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

        (ix) FEATURE:

                (D) OTHER INFORMATION:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

```
GTATGTGTCA GCCATGACCA CCCCGGCTCG TATGTCACCT GTAGATTTCC ACACGCCAAG   60

CTCCCCCAAA TCGCCCCCTT CGGAAATGTC TCCACCCGTG TCCAGCATGA CGGTGTCCAT  120

GCCTTCCATG GCGGTCAGCC CCTTCATGGA AGAAGAGAGA CCTCTACTTC TCGTGACACC  180

ACCAAGGCTG CGGGAGAAGA AGTTTGACCA TCACCCTCAG CAGTTCAGCT CCTTCCACCA  240

CAACCCCGCG CATGACAGTA ACAGCCTCCC TGCTAGCCCC TTGAGGATAG TGGAGGATGA  300

GGAGTATGAA ACGACCCAAG AGTACGAGCC AGCCCAAGAG CCTGTTAAGA AACTCGCCAA  360

TAGCCGGCGG GCCAAAAGAA CCAAGCCCAA TGGCCACATT GCTAACAGAT TGGAAGTGGA  420

CAGCAACACA AGCTCCCAGA GCAGTAACTC AGAGAGTGAA ACAGAAGATG AAAGAGTAGG  480

TGAAGATACG CCTTTCCTGG GCATACAGAA CCCCCTGGCA GCCAGTCTTG AGGCAACACC  540

TGCCTTCCGC CTGGCTGACA GCAGGACTAA CCCAGCAGGC CGCTTCTCGA CACAGGAAGA  600

AATCCAGGCC AGGCTGTCTA GTGTAATTGC TAACCAAGAC CCTATTGCTG TATAAAACCT  660

AAATAAACAC ATAGATTCAC CTGTAAAACT TTATTTTATA TAATAAAGTA TTCCACCTTA  720

AATTAAACAA                                                        730
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 78:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at positions 10 and 19 is C or
T; N at positions 1, 4 and 13 is A or G; N at positions 7 and 16
is A, T, G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

```
NCTNTCNGCN AANCTNGCNT T                                             21
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 79:

    (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear

        (ix) FEATURE:

                    (D) OTHER INFORMATION: N at position 19 is C or T; N at
positions 1, 4 and 13 is A or G; N at positions 7, 10 and 16 is
A, T, G or C.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

NCTNCTNGCN AGNCTNGCNT T   ·   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 80:

        (i) SEQUENCE CHARACTERISTICS:

                    (A) LENGTH: 20
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear

        (ix) FEATURE:

                    (D) OTHER INFORMATION: N at position 9 is A or G; N at
positions 3, 6, 17 and 18 is A, T, G or C.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

ACNACNGANA TGGCTCNNGA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 81:

        (i) SEQUENCE CHARACTERISTICS:

                    (A) LENGTH: 20
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear

        (ix) FEATURE:

                    (D) OTHER INFORMATION: N at position 16 is C or T; N at
position 9 is A or G; N at positions 3, 6 and 17 is A, T, G or C.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ACNACNGANA TGGCAGNNGA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 82:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at position 3 is C or T; N at
position 6 is A or G; N at positions 9, 15 and 18 is A, T, G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CANCANGTNT GGGCNGCNAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 83:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at position 3 is C or T; N at
position 15 is A or G; N at positions 9, 15 and 18 is A, T, G or
C; N at position 12 is A, C or T.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TTNGTNGTNA TNGANGGNAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 84:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

     (ix) FEATURE:

         (D) OTHER INFORMATION: N at positions 9 and 15 is C or T;
N at position 3 is A or G; N at positions 6, 12 and 18 is A, T, G
or C.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

AANGGNGANG CNCANACNGA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 85:

     (i) SEQUENCE CHARACTERISTICS:

         (A) LENGTH: 20
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

     (ix) FEATURE:

         (D) OTHER INFORMATION: N at positions 7 and 15 is C or T;
N at position 3 is A or G; N at positions 6, 9, 11, 14 and 17 is
A, T, G or C.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GANGCNNTNG CNGCNNTNAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 86:

     (i) SEQUENCE CHARACTERISTICS:

         (A) LENGTH: 20
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

     (ix) FEATURE:

         (D) OTHER INFORMATION: N at position 19 is C or T; N at
positions 15 and 18 is A or G; N at positions 3, 6, 9 and 12 is
A, T, G or C.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

GTNGGNTCNG TNCANGANNT   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 87:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at positions 9 and 19 is C or T;
N at positions 15 and 18 is A or G; N at positions 3, 6 and 12 is
A, T, G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

GTNGGNAGNG TNCANGANNT   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 88:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at positions 4, 7 and 16 is C
or T; N at position 12 is A or G; N at positions 1, 10 and 19 is
A, T, G or C; N at position 13 is A, G or T.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

NACNTTNTTN ANNATNTGNC C   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 89:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 417
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in positions 14, 23, 90, 100, 126,

-138-

and 135 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```
TCTAA AAC TAC AGA GAC TGT ATT TTC ATG ATC ATC ATA GTT CTG TGA AAT ATA  53
      Asn Tyr Arg Asp Cys Ile Phe Met Ile Ile Ile Val Leu Xaa Asn Ile
      1               5                   10                  15

CTT AAA CCG CTT TGG TCC TGA TCT TGT AGG AAG TCA GAA CTT CGC ATT         101
Leu Lys Pro Leu Trp Ser Xaa Ser Cys Arg Lys Ser Glu Leu Arg Ile
            20              25                  30

AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC         149
Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Ser Met Cys Lys Val Ile
            35              40                  45

AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG         197
Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Arg Ile Val Glu
            50              55                  60

TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA         245
Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg
65              70                  75                  80

GGA GTG ATC AAG GTA TGT GGT CAC ACT TGA ATC ACG CAG GTG TCT GAA         293
Gly Val Ile Lys Val Cys Gly His Thr Xaa Ile Thr Gln Val Ser Glu
            85                  90                  95

ATC TCA TTG TGA ACA AAT AAA AAT CAT GAA AGG AAA ACT CTA TGT TTG         341
Ile Ser Cys Xaa Thr Asn Lys Asn His Glu Arg Lys Thr Leu Cys Leu
            100                 105                 110

AAA TAT CTT ATG GGT CCT CCT GTA AAG CTC TTC ACT CCA TAA GGT GAA         389
Lys Tyr Leu Met Gly Pro Pro Val Lys Leu Phe Thr Pro Xaa Gly Glu
            115                 120                 125

ATA GAC CTG AAA TAT ATA TAG ATT ATT T                                   417
Ile Asp Leu Lys Tyr Ile Xaa Ile Ile
            130                 135
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 90:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

(D) OTHER INFORMATION: N in position 16 can be A or G; N
in position 22 can be A or G; N in position 28 can be C or T.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

CCGAATTCTG CAGGANACUC ANCCUGANCC UGG   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 91:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 37
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N in position 17 can be A or G; N in
position 26 can be A, G or T.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

AAGGATCCTG CAGUGTNTAU GCUCCNATUA CCATUGG   37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 92:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 34
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N in position 19 can be C or T; N in
position 28 can be A or G; N in position 31 can be C or T.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CCGAATTCTG CAGGCUGANT CUGGUGANTA NATG   34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 93:

    (i) SEQUENCE CHARACTERISTICS:

```
          (A)  LENGTH:           33
          (B)  TYPE:             nucleic acid
          (C)  STRANDEDNESS:     single
          (D)  TOPOLOGY:         linear

     (ix) FEATURE:

          (D)  OTHER INFORMATION:  N in position 19 can be C or T; N in
position 22 can be C or T; N in position 28 can be A or G; N in position
31 can be C or T.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CCGAATTCTG CAGGCUGANA GNGGUGANTA NAT                              33


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     94:

     (i) SEQUENCE CHARACTERISTICS:

          (A)  LENGTH:           34
          (B)  TYPE:             nucleic acid
          (C)  STRANDEDNESS:     single
          (D)  TOPOLOGY:         linear

     (ix) FEATURE:

          (D)  OTHER INFORMATION:  N in position 19 can be A or G; N in
position 22 can be C or T; N in position 32 can be A or G.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

AAGGATCCTG CAGUUUCATN TANTCUCCUG ANTC                             34


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     95:

     (i) SEQUENCE CHARACTERISTICS:

          (A)  LENGTH:           34
          (B)  TYPE:             nucleic acid
          (C)  STRANDEDNESS:     single
          (D)  TOPOLOGY:         linear

     (ix) FEATURE:

          (D)  OTHER INFORMATION:  N in position 20 can be A or G; N in
position 23 can be C or T; N in position 29 can be A or G; N in
position 32 can be A or G.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:
```

AAGGATCCTG CAGUUUCATN TANTCUCCNC TNTC   34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 96:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N in position 16 can be C or T; N in
position 19 can be A or G.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CCGAATTCTG CAGCANCANG TUTGGGCUGC TAA   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 97:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 35
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N in position 16 can be A or C or T;
N in position 19 can be C or T; N in position 22 can be C or T; N in
position 28 can be A or G; N in position 34 can be A or G.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CCGAATTCTG CAGATNTTNT TNATGGANCC UGANG   35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 98:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 35
        (B) TYPE: nucleic acid

```
        (C)  STRANDEDNESS:          single
        (D)  TOPOLOGY:              linear

    (ix)  FEATURE:

        (D)   OTHER INFORMATION:  N in position 30 can be C or T.

    (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 98:

CCGAATTCTG CAGGGGGUCC UCCUGCUTTN CCUGT                          35


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    99:

    (i)  SEQUENCE CHARACTERISTICS:

        (A)  LENGTH:               33
        (B)  TYPE:                 nucleic acid
        (C)  STRANDEDNESS:         single
        (D)  TOPOLOGY:             linear

    (ix)  FEATURE:

        (D)   OTHER INFORMATION:  N in position 19 can be C or T; N in
position 28 can be A or C or T; N in position 31 can be A or G.

    (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 99:

CCGAATTCTG CAGTGGTTNG TUGTUATNGA NGG                            33


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    100:

    (i)  SEQUENCE CHARACTERISTICS:

        (A)  LENGTH:               34
        (B)  TYPE:                 nucleic acid
        (C)  STRANDEDNESS:         single
        (D)  TOPOLOGY:             linear

    (ix)  FEATURE:

        (D)   OTHER INFORMATION:  N at position 17, 20, and 26 is
Inosinc.  Y can be cytidine or thymidine.

    (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO: 100:

AAGGATCCTG CAGYTTNGC NGCCCANACY TGRTG                           34


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    101:
```

(i) SEQUENCE CHARACTERISTICS:

      (A) LENGTH: 33
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

(ix) FEATURE:

      (D) OTHER INFORMATION: N in position 16 can be C or T; N in position 22 can be C or T; N in position 28 can be A or G; N in position 31 can be A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

AAGGATCCTG CAGGCNTCUG GNTCCATNAA NAA   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 102:

(i) SEQUENCE CHARACTERISTICS:

      (A) LENGTH: 33
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

(ix) FEATURE:

      (D) OTHER INFORMATION: N in position 19 can be A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

AAGGATCCTG CAGACUGGNA AUGCUGGUGG UCC   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 103:

(i) SEQUENCE CHARACTERISTICS:

      (A) LENGTH: 35
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

(ix) FEATURE:

      (D) OTHER INFORMATION: N in position 14 can be C or T; N in position 20 can be C or T; N in position 23 can be A or G or T; N in position 32 can be A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

AAGGATCCTG CAGNTTUCCN TCNATUACUA CNAAC   35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 104:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N in position 4 can be A or G; N in
position 7 cna be C or T; N in position 10 can be A or G; N in position
13 can be C or T.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CATNTANTCN TANTCTCUGC AAGGATCCTG CAG   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 105:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N in position 16 can be A or G; N
in position 22 can be C or T; N in position 28 can be C or T.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CCGAATTCTG CAGAANGGUG ANGCUCANAC UGA   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 106:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

     (ix) FEATURE:

         (D) OTHER INFORMATION: N in position 6 can be C or T; N in
position 12 can be C or T; N in position 15 can be C or T.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

GCUGCNAAUG CNTCNTTUGC AAGGATCCTG CAG   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 107:

     (i) SEQUENCE CHARACTERISTICS:

         (A) LENGTH: 33
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

     (ix) FEATURE:

         (D) OTHER INFORMATION: N in position 12 can be C or T; N in
position 15 can be C or T.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

GCUGCUAGUG CNTCNTTTGC AAGGATCCTG CAG   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 108:

     (i) SEQUENCE CHARACTERISTICS:

         (A) LENGTH: 30
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

     (ix) FEATURE:

         (D) OTHER INFORMATION: N in position 6 can be A or G; N in
position 9 can be A or G.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

TCUGCNAANT AUCCUGCAAG GATCCTGCAG   30

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 109:

                              -146-

(i) SEQUENCE CHARACTERISTICS:

      (A) LENGTH: 38
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CATCGATCTG CAGGCTGATT CTGGAGAATA TATGTGCA   38

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 110:

   (i) SEQUENCE CHARACTERISTICS:

      (A) LENGTH: 37
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

AAGGATCCTG CAGCCACATC TCGAGTCGAC ATCGATT   37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 111:

   (i) SEQUENCE CHARACTERISTICS:

      (A) LENGTH: 37
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CCGAATTCTG CAGTGATCAG CAAACTAGGA AATGACA   37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 112:

   (i) SEQUENCE CHARACTERISTICS:

      (A) LENGTH: 37
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

CATCGATCTG CAGCCTAGTT TGCTGATCAC TTTGCAC   37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 113:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 37
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

AAGGATCCTG CAGTATATTC TCCAGAATCA GCCAGTG   37

C\

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 114:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 34
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

AAGGATCCTG CAGGCACGCA GTAGGCATCT CTTA   34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 115:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 35
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

CCGAATTCTG CAGCAGAACT TCGCATTAGC AAAGC   35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 116:

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 33
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

CATCCCGGGA TGAAGAGTCA GGAGTCTGTG GCA   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 117:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 39
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATACCCGGGC TGCAGACAAT GAGATTTCAC ACACCTGCG   39

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 118:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 36
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

AAGGATCCTG CAGTTTGGAA CCTGCCACAG ACTCCT   36

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 119:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 39
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 120:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 12
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

His Gln Val Trp Ala Ala Lys Ala Ala Gly Leu Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 121:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 16
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Gly Gly Leu Lys Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Ala Asn
 1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 122:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 12 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser
 1   5   10   15

Cys Gly Arg Leu Lys Glu Asp
            20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(D)   OTHER INFORMATION: Xaa in position 10 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

```
Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu Ala Asn Ser
 1               5                  10                  15

Ser Gly Gly Pro Gly Arg Leu
              20
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 126:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 14
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

```
Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser
 1               5                  10
```

C¹

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 127:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 16
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```
Glu Tyr Lys Cys Leu Lys Phe Lys Trp Phe Lys Lys Ala Thr Val Met
 1               5                  10                  15
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 128:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 26
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

```
Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys
 1               5                  10                  15
```

Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys
            20   25

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 129:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 12 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 130:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 23
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met
 1   5   10   15

Cys Lys Val Ile Ser Lys Leu
            20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 131:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 12
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 132:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 22
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
1   5   10   15

Lys Val Ile Ser Lys Leu
            20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 133:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 744
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG 55
        His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu
        1   5   10   15

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC   103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys
        20   25   30

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG   151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu
        35   40   45

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC   199
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro
    50   55   60

TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG   247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val

-154-

```
CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG   295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu
                85                    90                    95

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA   343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu
            100                   105                   110

TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC   391
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser
            115                   120                   125

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG   439
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys
        130                   135                   140

TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT   487
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr
145                   150                   155                   160

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC   535
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn
                165                   170                   175

ATC ACC ATT GTG GAG TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT   583
Ile Thr Ile Val Glu Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile
                180                   185                   190

TCT CAG TCT CTA AGA GGA GTG ATC AAG GTA TGT GGT CAC ACT           625
Ser Gln Ser Leu Arg Gly Val Ile Lys Val Cys Gly His Thr
            195                   200                   205

TGAATCACGC AGGTGTGTGA AATCTCATTG TCAACAAATA AAAATCATGA AAGGAAAAAA 685

AAAAAAAAAA AATCGATGTC GACTCGAGAT GTGGCTGCAG GTCGACTCTA GAGGATCCC  744
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 134:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 1193
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

```
CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG 55
```

```
        His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu
        1               5               10              15

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC 103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys
            20              25              30

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG 151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu
            35              40              45

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC 199
Ala Lys Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro
        50              55              60

TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG 247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val
65              70              75              80

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG 295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu
            85              90              95

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA 343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu
            100             105             110

TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC 391
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser
            115             120             125

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG 439
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys
        130             135             140

TCA GGA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT 487
Ser Gly Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr
145             150             155             160

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC 535
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn
            165             170             175

ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA 583
Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr
            180             185             190

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 631
Ser His Leu Val Lys Ser Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
            195             200             205
```

-156-

```
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 679
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
    210             215             220

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 727
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
225             230             235             240

GTG CCC ATG AAA GTC CAA ACC CAA GAA AGT GCC CAA ATG AGT TTA CTG 775
Val Pro Met Lys Val Gln Thr Gln Glu Ser Ala Gln Met Ser Leu Leu
            245             250             255

GTG ATC GCT GCC AAA ACT ACG TAATGGCCAG CTTCTACAGT ACGTCCACTC   826
Val Ile Ala Ala Lys Thr Thr
            260

CCTTTCTGTC TCTGCCTGAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC 886

TCCCCTCAGA TTCCTCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT GACTGCCTCT 946

GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC CGTGACTAGT 1006

GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGTT TCTGAAATTG ATCTTGAATT 1066

ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG GCCTTGAAAA 1126

GTCAAAAAAA AAAAAAAAAA AAAAAATCGA TGTCGACTCG AGATGTGGCT GCAGGTCGAC 1186

TCTAGAG                                                         1193


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    135:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1108 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: cDNA
        (ix) FEATURE:

          (A) NAME/KEY: Coding Sequence
          (B) LOCATION: 8...778
          (D) OTHER INFORMATION:


        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

  CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC   49
          His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp
```

```
                1              5                    10

     TCG CTG CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC    97
     Ser Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro
     15              20              25                      30

     TCC TGC GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG   145
     Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu
                     35              40                      45

     CCC GAG GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT   193
     Pro Glu Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu
                     50              55                      60

     CCC CCC TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT   241
     Pro Pro Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly
                     65              70              75

     GCT GTG CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT   289
     Ala Val Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser
                 80              85              90

     CAG GAG TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT   337
     Gln Glu Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser
     95                  100             105                 110

     TCT GAA TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA   385
     Ser Glu Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu
                     115             120                 125

     TTA AGC CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG   433
     Leu Ser Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro
                 130             135                 140

     GGG AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA   481
     Gly Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly
                 145             150                 155

     GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT   529
     Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser
                 160             165                 170

     GCC AAC ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT   577
     Ala Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala
     175                 180                 185                 190

     GGG ACA AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT   625
     Gly Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys
                     195             200                 205

     GTG AAT GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA   673
```

-158-

```
Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser
            210                 215                 220

AGA TAC TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA   721
Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln
            225                 230                 235

AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT   769
Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser
    240                 245                 250

CTG CCT GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC TCCCCTCAG 827
Leu Pro Glu
255


ATTCCGCCTA GAGCTAGATG CGTTTTACCA GGTCTAACAT TGACTGCCTC TGCCTGTCGC  887
ATGAGAACAT TAACACAAGC GATTGTATGA CTTCCTCTGT CCGTGACTAG TGGGCTCTGA  947
GCTACTCGTA GGTGCGTAAG GCTCCAGTGT TTCTGAAATT GATCTTGAAT TACTGTGATA 1007
CGACATGATA GTCCCTCTCA CCCAGTGCAA TGACAATAAA GGCCTTGAAA AGTCAAAAAA 1067
AAAAAAAAAA AAAAAATCGA TGTCGACTCG AGATGTGGCT G                     1108
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 136:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 559
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: N in position 214 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```
AGTTTCCCCC CCCAACTTGT CGGAACTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC  60

GGCGGCTGCC CAGGCGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCCTCGGGC 120

TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC 180

CCAGCGGCGC GCCAGCAGGA GCCACCCCGC GAGNCGTGCG ACCGGGACGG AGCGCCCGCC 240

AGTCCCAGGT GGCCCGGACC GCACGTTGCG TCCCCGCGCT CCCCGCCGGC GACAGGAGAC 300

GCTCCCCCCC ACGCCGCGCG CGCCTCGGCC CGGTCGCTGG CCCGCCTCCA CTCCGGGGAC 360

AAACTTTTCC CGAAGCCGAT CCCAGCCCTC GGACCCAAAC TTGTCGCGCG TCGCCTTCGC 420
```

```
CGGGAGCCGT CCGCGCAGAG CGTGCACTTC TCGGGCGAG ATG TCG GAG CGC AGA    474
                                             Met Ser Glu Arg Arg
                                              1               5


GAA GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG    522
Glu Gly Lys Gly Lys Gly Lys Gly Gly Lys Lys Asp Arg Gly Ser Gly
                10                  15                  20


AAG AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA G                  559
Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala
                25                  30




(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     137:


    (i)  SEQUENCE CHARACTERISTICS:


        (A)  LENGTH:            252
        (B)  TYPE:              nucleic acid
        (C)  STRANDEDNESS:      single
        (D)  TOPOLOGY:          linear


    (ix) FEATURE:


        (D)  OTHER INFORMATION:  N in position 8 could be either
A or G.


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:



CC CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG     47
   His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser
    1           5                   10                  15

CTG CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC    95
Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser
                20                  25                  30

TGC GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC    143
Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro
                35                  40                  45

GAG GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC    191
Glu Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro
            50                  55                  60

CCC TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT    239
Pro Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala
            65                  70                  75




                              -160-
```

```
GTG CAA CGG TGC G                                                    252
Val Gln Arg Cys
 80
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 138:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 178
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

```
CCT TGC CTC CCC GCT TGA AAG AGA TGA AGA GTC AGG AGT CTG TGG CAG        48
Leu Pro Pro Arg Leu Lys Glu His Lys Ser Gln Glu Ser Val Ala Gly
 1               5                10                15

GTT CCA AAC TAG TGC TTC GGT GCG AGA CCA GTT CTG AAT ACT CCT CTC        96
Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu
            20                25                30

TCA AGT TCA AGT GGT TCA AGA ATG GGA GTG AAT TAA GCC GAA AGA ACA       144
Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys
        35                40                45

AAC CAC AAA ACA TCA AGA TAC AGA AAA GGC CGG G                         178
Pro Gly Asn Ile Lys Ile Gln Lys Arg Pro Gly
    50                55
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 139:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 122
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```
G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA         46
  Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly
   1               5                10                15
```

```
GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT    94
Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser
                20                  25                  30

GCC AAC ATC ACC ATT GTG GAG TCA AAC G                             122
Ala Asn Ile Thr Ile Val Glu Ser Asn Ala
            35
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 140:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 417
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```
TCTAAAACTA CAGAGACTGT ATTTTCATGA TCATCATAGT TCTGTGAAAT ATACTTAAAC   60

CGCTTTGGTC CTGATCTTGT AGG AAG TCA GAA CTT CGC ATT AGC AAA GCG     110
                         Lys Ser Glu Leu Arg Ile Ser Lys Ala
                          1                   5

TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA   158
Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu
 10                  15                  20                  25

GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC GGT   206
Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Gly
                30                  35                  40

AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA GGA GTG ATC   254
Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg Gly Val Ile
                45                  50                  55

AAG GTA TGT GGT CAC ACT TGAATCACGC AGGTGTGTGA AATCTCATTG          302
Lys Val Cys Gly His Thr
                60

TGAACAAATA AAAATCATGA AAGGAAAACT CTATGTTTGA AATATCTTAT GGGTCCTCCT 362

GTAAAGCTCT TCACTCCATA AGGTGAAATA GACCTGAAAT ATATATAGAT TATTT       417
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 141:

    (i) SEQUENCE CHARACTERISTICS:

```
          (A)  LENGTH:            102
          (B)  TYPE:              nucleic acid
          (C)  STRANDEDNESS:      single
          (D)  TOPOLOGY:          linear

     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 141:

  AG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT       47
  Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser
  1               5                   10                  15

TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT       95
Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr
            20                  25                  30

TCT TCA T                                                             102
Ser Ser Ser
        35
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 142:

     (i) SEQUENCE CHARACTERISTICS:

```
          (A)  LENGTH:            69
          (B)  TYPE:              nucleic acid
          (C)  STRANDEDNESS:      single
          (D)  TOPOLOGY:          linear
```

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

```
AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT GTG CCC       48
Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro
1               5                   10                  15

ATG AAA GTC CAA ACC CAA GAA                                           69
Met Lys Val Gln Thr Gln Glu
            20
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 143:

     (i) SEQUENCE CHARACTERISTICS:

```
          (A)  LENGTH:            60
          (B)  TYPE:              nucleic acid
```

```
        (C) STRANDEDNESS:        single
        (D) TOPOLOGY:            linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:


AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG        48
Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met
 1               5                  10                 15

GCC AGC TTC TAC                                                       60
Ala Ser Phe Tyr
             20



(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    144:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH:             36
        (B) TYPE:               nucleic acid
        (C) STRANDEDNESS:       single
        (D) TOPOLOGY:           linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:


AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAG                       36
Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
 1               5                  10



(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    145:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH:             27
        (B) TYPE:               nucleic acid
        (C) STRANDEDNESS:       single
        (D) TOPOLOGY:           linear



    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

AAG CAT CTT GGG ATT GAA TTT ATG GAG                                   27
Lys His Leu Gly Ile Glu Phe Met Glu
 1               5



(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    146:
```

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 569
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

```
AAA GCG GAG GAG CTC TAC CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT      48
Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile
 1               5                  10                  15

TGC ATC GCG CTG CTC GTG GTT GGC ATC ATG TGT GTG GTG GTC TAC TGC      96
Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val Val Tyr Cys
                20                  25                  30

AAA ACC AAG AAA CAA CGG AAA AAG CTT CAT GAC CGG CTT CGG CAG AGC     144
Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg Gln Ser
            35                  40                  45

CTT CGG TCT GAA AGA AAC ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC     192
Leu Arg Ser Glu Arg Asn Thr Met Met Asn Val Ala Asn Gly Pro His
        50                  55                  60

CAC CCC AAT CCG CCC CCC GAG AAC GTG CAG CTG GTG AAT CAA TAC GTA     240
His Pro Asn Pro Pro Pro Glu Asn Val Gln Leu Val Asn Gln Tyr Val
 65                  70                  75                  80

TCT AAA AAT GTC ATC TCT AGC GAG CAT ATT GTT GAG AGA GAG GCG GAG     288
Ser Lys Asn Val Ile Ser Ser Glu His Ile Val Glu Arg Glu Ala Glu
                85                  90                  95

AGC TCT TTT TCC ACC AGT CAC TAC ACT TCG ACA GCT CAT CAT TCC ACT     336
Ser Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Ala His His Ser Thr
                100                 105                 110

ACT GTC ACT CAG ACT CCC AGT CAC AGC TGG AGC AAT GGA CAC ACT GAA     384
Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly His Thr Glu
                115                 120                 125

AGC ATC ATT TCG GAA AGC CAC TCT GTC ATC GTG ATG TCA TCC GTA GAA     432
Ser Ile Ile Ser Glu Ser His Ser Val Ile Val Met Ser Ser Val Glu
    130                 135                 140

AAC AGT AGG CAC AGC AGC CCG ACT GGG GGC CCG AGA GGA CGT CTC AAT     480
Asn Ser Arg His Ser Ser Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn
145                 150                 155                 160

GGC TTG GGA GGC CCT CGT GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA     528
Gly Leu Gly Gly Pro Arg Glu Cys Asn Ser Phe Leu Arg His Ala Arg
```

-165-

```
GAA ACC CCT GAC TCC TAC CGA GAC TCT CCT CAT AGT G AAAG          569
Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser
        180                 185
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 147:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 730
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

```
G TAT GTA TCA GCA ATG ACC ACC CCG GCT CGT ATG TCA CCT GTA GAT    46
  Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro Val Asp
   1               5                  10                  15

TTC CAC ACG CCA AGC TCC CCC AAG TCA CCC CCT TCG GAA ATG TCC CCG   94
Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro Ser Glu Met Ser Pro
                20              25              30

CCC GTG TCC AGC ACG ACG GTC TCC ATG CCC TCC ATG GCG GTC AGT CCC  142
Pro Val Ser Ser Thr Thr Val Ser Met Pro Ser Met Ala Val Ser Pro
            35              40              45

TTC GTG GAA GAG GAG AGA CCC CTG CTC CTT GTG ACG CCA CCA CGG CTG  190
Phe Val Glu Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu
        50              55              60

CGG GAG AAG TAT GAC CAC CAC GCC CAG CAA TTC AAC TCG TTC CAC TGC  238
Arg Glu Lys Tyr Asp His His Ala Gln Gln Phe Asn Ser Phe His Cys
     65              70              75

AAC CCC GCG CAT GAG AGC AAC AGC CTG CCC CCC AGC CCC TTG AGG ATA  286
Asn Pro Ala His Glu Ser Asn Ser Leu Pro Pro Ser Pro Leu Arg Ile
 80              85              90              95

GTG GAG GAT GAG GAA TAT GAA ACG ACC CAG GAG TAC GAA CCA GCT CAA  334
Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala Gln
            100             105             110

GAG CCG GTT AAG AAA CTC ACC AAC AGC AGC CGG CGG GCC AAA AGA ACC  382
Glu Pro Val Lys Lys Leu Thr Asn Ser Ser Arg Arg Ala Lys Arg Thr
            115             120             125
```

```
AAG CCC AAT GGT CAC ATT GCC CAC AGG TTG GAA ATG GAC AAC AAC ACA      430
Lys Pro Asn Gly His Ile Ala His Arg Leu Glu Met Asp Asn Asn Thr
        130             135             140

GGC GCT GAC AGC AGT AAC TCA GAG AGC GAA ACA GAG GAT GAA AGA GTA      478
Gly Ala Asp Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp Glu Arg Val
        145             150             155

GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG AAC CCC CTG GCA GCC AGT      526
Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln Asn Pro Leu Ala Ala Ser
160             165             170             175

CTC GAG GCG GCC CCT GCC TTC CGC CTG GTC GAC AGC AGG ACT AAC CCA      574
Leu Glu Ala Ala Pro Ala Phe Arg Leu Val Asp Ser Arg Thr Asn Pro
            180             185             190

ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG CAG GCC AGG CTC TCC GGT      622
Thr Gly Gly Phe Ser Pro Gln Glu Glu Leu Gln Ala Arg Leu Ser Gly
        195             200             205

GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC TAAAACCGAA ATACACCCAT       672
Val Ile Ala Asn Gln Asp Pro Ile Ala Val
        210             215

AGATTCACCT GTAAAACTTT ATTTTATATA ATAAAGTATT CCACCTTAAA TTAAACAA     730
```

C^1

```
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     148:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1652 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: cDNA
        (ix) FEATURE:

          (A) NAME/KEY: Coding Sequence
          (B) LOCATION: 459...1181
          (D) OTHER INFORMATION:


        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

AGTTTCCCCC CCCAACTTGT CGGAACTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC  60
GGCGGCTGCC CAGGCGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCCTCGGGC 120
TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC 180
CCAGCGGCGC GCCAGCAGGA GCCACCCCGC GAGCGTGCGA CCGGGACGGA GCGCCCGCCA 240
GTCCCAGGTG GCCCGGACCG CACGTTGCGT CCCCGCGCTC CCCGCCGGCG ACAGGAGACG 300
```

-167-

CTCCCCCCCA CGCCGCGCGC GCCTCGGCCC GGTCGCTGGC CCGCCTCCAC TCCGGGGACA 360
AACTTTTCCC GAAGCCGATC CCAGCCCTCG GACCCAAACT TGTCGCGCGT CGCCTTCGCC 420
GGGAGCCGTC CGCGCAGAGC GTGCACTTCT CGGGCGAG ATG TCG GAG CGC AGA GAA 476
                                          Met Ser Glu Arg Arg Glu
                                          1   5

GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG AAG   524
Gly Lys Gly Lys Gly Lys Gly Gly Lys Lys Asp Arg Gly Ser Gly Lys
            10   15   20

AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA GCC TTG CCT CCC CGC   572
Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala Leu Pro Pro Arg
        25   30   35

TTG AAA GAG ATG AAG ATG CAG GAG TCT GTG GCA GGT TCC AAA CTA GTG   620
Leu Lys Glu Met Lys Met Gln Glu Ser Val Ala Gly Ser Lys Leu Val
    40   45   50

CTT CGG TGC GAG ACC AGT TCT GAA TAC TCC TCT CTC AAG TTC AAG TGG   668
Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Lys Phe Lys Trp
55   60   65   70

TTC AAG AAT GGG AGT GAA TTA AGC CGA AAG AAC AAA CCA CAA AAC ATC   716
Phe Lys Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys Pro Gln Asn Ile
                75   80   85

AAG ATA CAG AAA AGG CCG GGG AAG TCA GAA CTT CGC ATT AGC AAA GCG   764
Lys Ile Gln Lys Arg Pro Gly Lys Ser Glu Leu Arg Ile Ser Lys Ala
                90   95   100

TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA   812
Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu
            105   110   115

GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC GAG   860
Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Glu
        120   125   130

ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT TCA   908
Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser Ser
135   140   145   150

GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT TCT   956
Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr Ser
                155   160   165

TCA TCC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG TGT   1004
Ser Ser Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys Cys
            170   175   180

GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC ATG   1052

-168-

```
        Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met
            185          .              190             195

        GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG TGC AAG TGC CCA AAT   1100
        Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn
            200                     205             210

        GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC   1148
        Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr
        215                     220             225             230

        AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAGGCGCATG CTCAGTCGGT 1201
        Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
                        235             240
```

```
        GCCGCTTTCT TGTTGCCGCA TCTCCCCTCA GATTCAACCT AGAGCTAGAT GCGTTTTACC 1261
        AGGTCTAACA TTGACTGCCT CTGCCTGTCG CATGAGAACA TTAACACAAG CGATTGTATG 1321
        ACTTCCTCTG TCCGTGACTA GTGGGCTCTG AGCTACTCGT AGGTGCGTAA GGCTCCAGTG 1381
        TTTCTGAAAT TGATCTTGAA TTACTGTGAT ACGACATGAT AGTCCCTCTC ACCCAGTGCA 1441
        ATGACAATAA AGGCCTTGAA AAGTCTCACT TTTATTGAGA AAATAAAAAT CGTTCCACGG 1501
        GACAGTCCCT CTTCTTTATA AAATGACCCT ATCCTTGAAA AGGAGGTGTG TTAAGTTGTA 1561
        ACCAGTACAC ACTTGAAATG ATGGTAAGTT CGCTTCGGTT CAGAATGTGT TCTTTCTGAC 1621
        AAATAAACAG AATAAAAAAA AAAAAAAAAA A                                1652
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 149:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 1140
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```
CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG 48
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu
1               5               10              15

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC 96
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys
            20              25              30

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG 144
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu
            35              40              45

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC 192
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro
    50              55              60
```

TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG 240
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val
65   70   75   80

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG 288
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu
                85   90   95

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA 336
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu
            100   105   110

TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC 384
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser
            115   120   125

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG 432
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys
        130   135   140

TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT 480
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr
145   150   155   160

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC 528
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn
            165   170   175

ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA 576
Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr
            180   185   190

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 624
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
            195   200   205

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 672
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
        210   215   220

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 720
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
225   230   235   240

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT 768
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr
            245   250   255

GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC 816
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser
            260   265   270

-170-

```
ACT CCC TTT CTG TCT CTG CCT GAA  TAGCGCATCT CAGTCGGTGC CGCTTTCTTG 870
Thr Pro Phe Leu Ser Leu Pro Glu
        275                 280


TTGCCGCATC TCCCCTCAGA TTCCNCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT 930

GACTGCCTCT GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC 990

CGTGACTAGT GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGTT TCTGAAATTG 1050

ATCTTGAATT ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG 1110

GCCTTGAAAA GTCAAAAAAA AAAAAAAAAA                                  1140


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    150:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH:              1764
        (B) TYPE:                nucleic acid
        (C) STRANDEDNESS:        single


        (D) TOPOLOGY:            linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:


G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA   49
  Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu
   1               5                  10                  15

TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC    97
Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala
            20                  25                  30

AAC ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG   145
Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly
            35                  40                  45

ACA AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG   193
Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val
    50                  55                  60

AAT GGA GGC GAC TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA   241
Asn Gly Gly Asp Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg
65                  70                  75                  80

TAC TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG   289
Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu
```

-171-

```
AAT GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC    337
Asn Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr
        100             105             110
```

```
CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT TGC ATC GCG CTG CTC GTG    385
Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val
        115             120             125
```

```
GTT GGC ATC ATG TGT GTG GTG GTC TAC TGC AAA ACC AAG AAA CAA CGG    433
Val Gly Ile Met Cys Val Val Val Tyr Cys Lys Thr Lys Lys Gln Arg
        130             135             140
```

```
AAA AAG CTT CAT GAC CGG CTT CGG CAG AGC CTT CGG TCT GAA AGA AAC    481
Lys Lys Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn
145             150             155             160
```

```
ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC CAC CCC AAT CCG CCC CCC    529
Thr Met Met Asn Val Ala Asn Gly Pro His His Pro Asn Pro Pro Pro
                165             170             175
```

```
GAG AAC GTG CAG CTG GTG AAT CAA TAC GTA TCT AAA AAT GTC ATC TCT    577
Glu Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser
                180             185             190
```

```
AGC GAG CAT ATT GTT GAG AGA GAG GCG GAG AGC TCT TTT TCC ACC AGT    625
Ser Glu His Ile Val Glu Arg Glu Ala Glu Ser Ser Phe Ser Thr Ser
                195             200             205
```

```
CAC TAC ACT TCG ACA GCT CAT CAT TCC ACT ACT GTC ACT CAG ACT CCC    673
His Tyr Thr Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro
        210             215             220
```

```
AGT CAC AGC TGG AGC AAT GGA CAC ACT GAA AGC ATC ATT TCG GAA AGC    721
Ser His Ser Trp Ser Asn Gly His Thr Glu Ser Ile Ile Ser Glu Ser
225             230             235             240
```

```
CAC TCT GTC ATC GTG ATG TCA TCC GTA GAA AAC AGT AGG CAC AGC AGC    769
His Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser
                245             250             255
```

```
CCG ACT GGG GGC CCG AGA GGA CGT CTC AAT GGC TTG GGA GGC CCT CGT    817
Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly Leu Gly Gly Pro Arg
                260             265             270
```

```
GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA GAA ACC CCT GAC TCC TAC    865
Glu Cys Asn Ser Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr
                275             280             285
```

```
CGA GAC TCT CCT CAT AGT GAA AGA CAT AAC CTT ATA GCT GAG CTA AGG    913
Arg Asp Ser Pro His Ser Glu Arg His Asn Leu Ile Ala Glu Leu Arg
        290             295             300

AGA AAC AAG GCC CAC AGA TCC AAA TGC ATG CAG ATC CAG CTT TCC GCA    961
Arg Asn Lys Ala His Arg Ser Lys Cys Met Gln Ile Gln Leu Ser Ala
305             310             315             320

ACT CAT CTT AGA GCT TCT TCC ATT CCC CAT TGG GCT TCA TTC TCT AAG   1009
Thr His Leu Arg Ala Ser Ser Ile Pro His Trp Ala Ser Phe Ser Lys
                325             330             335

ACC CCT TGG CCT TTA GGA AGG TAT GTA TCA GCA ATG ACC ACC CCG GCT   1057
Thr Pro Trp Pro Leu Gly Arg Tyr Val Ser Ala Met Thr Thr Pro Ala
            340             345             350

CGT ATG TCA CCT GTA GAT TTC CAC ACG CCA AGC TCC CCC AAG TCA CCC   1105
Arg Met Ser Pro Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro
        355             360             365

CCT TCG GAA ATG TCC CCG CCC GTG TCC AGC ACG ACG GTC TCC ATG CCC   1153
Pro Ser Glu Met Ser Pro Pro Val Ser Ser Thr Thr Val Ser Met Pro
        370             375             380

TCC ATG GCG GTC AGT CCC TTC GTG GAA GAG GAG AGA CCC CTG CTC CTT   1201
Ser Met Ala Val Ser Pro Phe Val Glu Glu Glu Arg Pro Leu Leu Leu
385             390             395             400

GTG ACG CCA CCA CGG CTG CGG GAG AAG TAT GAC CAC CAC GCC CAG CAA   1249
Val Thr Pro Pro Arg Leu Arg Glu Lys Tyr Asp His His Ala Gln Gln
            405             410             415

TTC AAC TCG TTC CAC TGC AAC CCC GCG CAT GAG AGC AAC AGC CTG CCC   1297
Phe Asn Ser Phe His Cys Asn Pro Ala His Glu Ser Asn Ser Leu Pro
            420             425             430

CCC AGC CCC TTG AGG ATA GTG GAG GAT GAG GAA TAT GAA ACG ACC CAG   1345
Pro Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln
            435             440             445

GAG TAC GAA CCA GCT CAA GAG CCG GTT AAG AAA CTC ACC AAC AGC AGC   1393
Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys Leu Thr Asn Ser Ser
450             455             460

CGG CGG GCC AAA AGA ACC AAG CCC AAT GGT CAC ATT GCC CAC AGG TTG   1441
Arg Arg Ala Lys Arg Thr Lys Pro Asn Gly His Ile Ala His Arg Leu
465             470             475             480

GAA ATG GAC AAC AAC ACA GGC GCT GAC AGC AGT AAC TCA GAG AGC GAA   1489
Glu Met Asp Asn Asn Thr Gly Ala Asp Ser Ser Asn Ser Glu Ser Glu
                485             490             495
```

```
ACA GAG GAT GAA AGA GTA GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG    1537
Thr Glu Asp Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln
            500                 505                 510

AAC CCC CTG GCA GCC AGT CTC GAG GCG GCC CCT GCC TTC CGC CTG GTC    1585
Asn Pro Leu Ala Ala Ser Leu Glu Ala Ala Pro Ala Phe Arg Leu Val
            515                 520                 525

GAC AGC AGG ACT AAC CCA ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG    1633
Asp Ser Arg Thr Asn Pro Thr Gly Gly Phe Ser Pro Gln Glu Glu Leu
            530                 535                 540

CAG GCC AGG CTC TCC GGT GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC    1681
Gln Ala Arg Leu Ser Gly Val Ile Ala Asn Gln Asp Pro Ile Ala Val
545                 550                 555                 560

TAAAACCGAA ATACACCCAT AGATTCACCT GTAAAACTTT ATTTTATATA ATAAAGTATT 1741

CCACCTTAAA TTAAACAAAA AAA                                          1764
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 151:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 50
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

```
Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
 1               5               10                  15

Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
            20                  25                  30

Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser
            35                  40                  45

Phe Tyr
    50
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 152:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 50
        (B) TYPE: amino acid

```
        (C)  STRANDEDNESS:
        (D)  TOPOLOGY:              linear


   (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
 1               5                   10                   15


Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
            20                  25                  30


Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro Met Lys
        35                  40                  45


Val Gln
    50


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    153:

   (i)  SEQUENCE CHARACTERISTICS:

        (A)  LENGTH:              46
        (B)  TYPE:                amino acid
        (C)  STRANDEDNESS:
        (D)  TOPOLOGY:            linear


   (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 153:

Glu Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile His Gly Glu Cys Lys
 1               5                   10                   15


Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys Lys Cys Gln Gln Glu Tyr
            20                  25                  30


Phe Gly Glu Arg Cys Gly Glu Lys Ser Asn Lys Thr His Ser
        35                  40                  45



(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    154:

   (i)  SEQUENCE CHARACTERISTICS:

        (A)  LENGTH:              198
        (B)  TYPE:                nucleic acid
        (C)  STRANDEDNESS:        single
        (D)  TOPOLOGY:            linear


   (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 154:
```

```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1               5                   10                  15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
            20                  25                  30

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC 144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
            35                  40                  45

GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT 192
Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro
    50                  55                  60

GAA TAG                                                         198
Glu
65
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 155:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 192
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1               5                   10                  15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
            20                  25                  30

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
            35                  40                  45

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC TAA 192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr
    50                  55                  60
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 156:

(i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 183
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1   5   10   15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
            20   25   30

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC 144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
            35   40   45

GTA ATG GCC AGC TTC TAC AAA GCG GAG GAG CTC TAC TAA   183
Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr
        50   55   60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 157:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 210
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1   5   10   15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
            20   25   30

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC 144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
            35   40   45

-177-

```
GTA ATG GCC AGC TTC TAC AAG CAT CTT GGG ATT GAA TTT ATG GAG AAA 192
Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Lys
    50                  55                  60

GCG GAG GAG CTC TAC TAA                                          210
Ala Glu Glu Leu Tyr
65
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 158:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 267
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158: .

```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1               5                   10                  15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
            20                  25                  30

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
            35                  40                  45

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT 192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr
            50                  55                  60

GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC 240
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser
65                  70                  75                  80

ACT CCC TTT CTG TCT CTG CCT GAA TAG                             267
Thr Pro Phe Leu Ser Leu Pro Glu
                85
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 159:

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 252
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1               5                   10                  15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
            20                  25                  30

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
        35                  40                  45

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT 192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr
    50                  55                  60

GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AAA GCG GAG 240
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys Ala Glu
65                  70                  75                  80

GAG CTC TAC TAA                                              252
Glu Leu Tyr
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 160:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 128
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

```
CC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG TGT GCA    47
   Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys Cys Ala
   1               5                   10                  15

GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC ATG GTG    95
Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val
```

```
                    20                  25                   30
AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG T GC                      128
Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu
            35                  40
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 161:

     (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 141
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

C|

```
A CAT AAC CTT ATA GCT GAG CTA AGG AGA AAC AAG GCC CAC AGA TCC      46
  His Asn Leu Ile Ala Glu Leu Arg Arg Asn Lys Ala His Arg Ser
   1           5                  10                   15

AAA TGC ATG CAG ATC CAG CTT TCC GCA ACT CAT CTT AGA GCT TCT TCC   94
Lys Cys Met Gln Ile Gln Leu Ser Ala Thr His Leu Arg Ala Ser Ser
                20                  25                   30

ATT CCC CAT TGG GCT TCA TTC TCT AAG ACC CCT TGG CCT TTA GGA AG   141
Ile Pro His Trp Ala Ser Phe Ser Lys Thr Pro Trp Pro Leu Gly Arg
                35                  40                   45
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 162:

     (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 24
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

     (ix) FEATURE:

          (D)   OTHER INFORMATION: Xaa in positions 15 and 22 is
unknown.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

```
Ala Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Xaa Phe
 1           5                  10                   15
```

Met Val Lys Asp Leu Xaa Asn Pro
                    20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 163:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 745
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

ATG AGA TGG CGA CGC GCC CCG CGC CGC TCC GGG CGT CCC GGC CCC CGG 48
Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg
1   5   10   15

GCC CAG CGC CCC GGC TCC GCC GCC CGC TCG TCG CCG CCG CTG CCG CTG 96
Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu
                20   25   30

CTG CCA CTA CTG CTG CTG CTG GGG ACC GCG GCC CTG GCG CCG GGG GCG 144
Leu Pro Leu Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala
            35   40   45

GCG GCC GGC AAC GAG GCG GCT CCC GCG GGG GCC TCG GTG TGC TAC TCG 192
Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser
        50   55   60

TCC CCG CCC AGC GTG GGA TCG GTG CAG GAG CTA GCT CAG CGC GCC GCG 240
Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala
65   70   75   80

GTG GTG ATC GAG GGA AAG GTG CAC CCG CAG CGG CGG CAG CAG GGG GCA 288
Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala
                85   90   95

CTC GAC AGG AAG GCG GCG GCG GCG GCG GGC GAG GCA GGG GCG TGG GGC 336
Leu Asp Arg Lys Ala Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly
                100   105   110

GGC GAT CGC GAG CCG CCA GCC GCG GGC CCA CGG GCG CTG GGG CCG CCC 384
Gly Asp Arg Glu Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro
            115   120   125

GCC GAG GAG CCG CTG CTC GCC GCC AAC GGG ACC GTG CCC TCT TGG CCC 432
Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro

-181-

```
          130                    135                    140
ACC GCC CCG GTG CCC AGC GCC GGC GAG CCC GGG GAG GAG GCG CCC TAT 480
Thr Ala Pro Val Pro Ser Ala Gly Glu Pro Gly Glu Glu Ala Pro Tyr
145                    150                    155                    160

CTG GTG AAG GTG CAC CAG GTG TGG GCG GTG AAA GCC GGG GGC TTG AAG 528
Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys
                       165                    170                    175

AAG GAC TCG CTG CTC ACC GTG CGC CTG GGG ACC TGG GGC CAC CCC GCC 576
Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala
                       180                    185                    190

TTC CCC TCC TGC GGG AGG CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC 624
Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe
                       195                    200                    205

ATG GAG CCC GAC GCC AAC AGC ACC AGC CGC GCG CCG GCC GCC TTC CGA 672
Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Ala Phe Arg
          210                    215                    220

GCC TCT TTC CCC CCT CTG GAG ACG GGC CGG AAC CTC AAG AAG GAG GTC 720
Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Lys Glu Val
225                    230                    235                    240

AGC CGG GTG CTG TGC AAG CGG TGC G                                 745
Ser Arg Val Leu Cys Lys Arg Cys
                       245
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 164:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 12
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: Xaa in position 1 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

```
Xaa Ala Leu Ala Ala Ala Gly Tyr Asp Val Glu Lys
  1               5                  10
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 165:

```
        (i) SEQUENCE CHARACTERISTICS:

            (A)  LENGTH:              5
            (B)  TYPE:               amino acid
            (C)  STRANDEDNESS:
            (D)  TOPOLOGY:           linear

        (ix) FEATURE:

            (D)  OTHER INFORMATION:  Xaa in position 1 is unknown.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

Xaa Leu Val Leu Arg
  1               5
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 166:

```
        (i) SEQUENCE CHARACTERISTICS:

            (A)  LENGTH:             11
            (B)  TYPE:               amino acid
            (C)  STRANDEDNESS:
            (D)  TOPOLOGY:           linear

        (ix) FEATURE:

            (D)  OTHER INFORMATION:  Xaa in positions 1, 2, and 3 is
unknown.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Xaa Xaa Xaa Tyr Pro Gly Gln Ile Thr Ser Asn
  1               5                  10
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 167:

```
        (i) SEQUENCE CHARACTERISTICS:

            (A)  LENGTH:             60
            (B)  TYPE:               nucleic acid
            (C)  STRANDEDNESS:       single
            (D)  TOPOLOGY:           linear

        (ix)  FEATURE:

            (D)  OTHER INFORMATION: N in positions 25 and 36 is unknown.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:
```

ATAGGGAAGG GCGGGGGAAG GGTCNCCCTC NGCAGGGCCG GGCTTGCCTC TGGAGCCTCT   60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 168:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 18
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: N in position 16 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

TTTACACATA TATTCNCC   18

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 169:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 21
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

Glu Thr Gln Pro Asp Pro Gly Gln Ile Leu Lys Lys Val Pro Met Val
 1   5   10   15

Ile Gly Ala Tyr Thr
            20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 170:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 422
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

```
Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg
 1               5                  10                  15

Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu
            20                  25                  30

Leu Pro Leu Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala
        35                  40                  45

Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser
    50                  55                  60

Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala
65                  70                  75                  80

Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala
            85                  90                  95

Leu Asp Arg Lys Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly
            100                 105                 110

Gly Asp Arg Glu Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro
        115                 120                 125

Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro
    130                 135                 140

Thr Ala Pro Val Pro Ser Ala Gly Glu Pro Gly Glu Glu Ala Pro Tyr
145                 150                 155                 160

Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys
            165                 170                 175

Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala
            180                 185                 190

Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe
        195                 200                 205

Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Ala Phe Arg
    210                 215                 220

Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Lys Glu Val
225                 230                 235                 240

Ser Arg Val Leu Cys Lys Arg Cys Ala Leu Pro Pro Gln Leu Lys Glu
            245                 250                 255

Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu Val Leu Arg Cys
            260                 265                 270
```

```
Glu Thr Ser Ser Glu Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys Asn
        275              280              285

Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn Ile Lys Ile Gln
    290              295              300

Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile Asn Lys Ala Ser Leu Ala
305              310              315              320

Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp
                325              330              335

Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr
        340              345              350

Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys
        355              360              365

Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser
    370              375              380

Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp
385              390              395              400

Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro
                405              410              415

Phe Leu Ser Leu Pro Glu
            420


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     171:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH:              69
        (B) TYPE:                amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY:            linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
 1            5               10              15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
            20              25              30

Pro Arg Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr
            35              40              45
```

-186-

Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala
    50   55   60

Asn Thr Ser Ser Ser
 65

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 172:

    (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 19
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Arg Lys Gly Asp Val Pro Gly Pro Arg Val Lys Ser Ser Arg Ser Thr
 1   5   10   15

Thr Thr Ala

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 173:

    (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 231
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

CGCGAGCGCC TCAGCGCGGC CGCTCGCTCT CCCCCTCGAG GGACAAACTT TTCCCAAACC 60

CGATCCGAGC CCTTGGACCA AACTCGCCTG CGCCGAGAGC CGTCCGCGTA GAGCGCTCCG 120

TCTCCGGCGA GATGTCCGAG CGCAAAGAAG GCAGAGGCAA AGGGAAGGGC AAGAAGAAGG 180

AGCGAGGCTC CGGCAAGAAG CCGGAGTCCG CGGCGGGCAG CCAGAGCCCA G   231

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 174:

    (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 178
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

CCTTGCCTCC CCGATTGAAA GAGATGAAAA GCCAGGAATC GGCTGCAGGT TCCAAACTAG 60

TCCTTCGGTG TGAAACCAGT TCTGAATACT CCTCTCTCAG ATTCAAGTGG TTCAAGAATG 120

GGAATGAATT GAATCGAAAA AACAAACCAC AAAATATCAA GATACAAAAA AAGCCAGG   178

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 175:

        (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 122
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

GAAGTCAGAA CTTCGCATTA ACAAAGCATC ACTGGCTGAT TCTGGAGAGT ATATGTGCAA 60

AGTGATCAGC AAATTAGGAA ATGACAGTGC CTCTGCCAAT ATCACCATCG TGGAATCAAA 120

CG   122

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 176:

        (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 102
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

AGATCATCAC TGGTATGCCA GCCTCAACTG AAGGAGCATA TGTGTCTTCA GAGTCTCCCA 60

TTAGAATATC AGTATCCACA GAAGGAGCAA ATACTTCTTC AT   102

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 177:

        (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 128

(B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

CTACATCTAC ATCCACCACT GGGACAAGCC ATCTTGTAAA ATGTGCGGAG AAGGAGAAAA 60

CTTTCTGTGT GAATGGAGGG GAGTGCTTCA TGGTGAAAGA CCTTTCAAAC CCCTCGAGAT 120

ACTTGTGC   128

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 178:

       (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 69
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

AAGTGCCAAC CTGGATTCAC TGGAGCAAGA TGTACTGAGA ATGTGCCCAT GAAAGTCCAA 60

AACCAAGAA   69

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 179:

       (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 23
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

TCGGGCTCCA TGAAGAAGAT GTA   23

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 180:

       (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 23
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

TCCATGAAGA AGATGTACCT GCT   23

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 181:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 22
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ATGTACCTGC TGTCCTCCTT GA   22

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 182:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 22
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

TTGAAGAAGG ACTCGCTGCT CA   22

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 183:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

AAAGCCGGGG GCTTGAAGAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 184:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20
        (B) TYPE: nucleic acid

```
                (C)  STRANDEDNESS:           single
                (D)  TOPOLOGY:               linear

        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 184:

ATGARGTGTG GGCGGCGAAA                                              20

(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:      185:

        (i)  SEQUENCE CHARACTERISTICS:

                (A)  LENGTH:                 15
                (B)  TYPE:                   amino acid
                (C)  STRANDEDNESS:
                (D)  TOPOLOGY:               linear

        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 185:

Glu Gly Lys Val His Pro Gln Arg Arg Gly Ala Leu Asp Arg Lys
                     5                  10



(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:      186:

        (i)  SEQUENCE CHARACTERISTICS:
                (A)  LENGTH:                 17
                (B)  TYPE:                   amino acid
                (C)  STRANDEDNESS:
                (D)  TOPOLOGY:               linear

        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu
                     5                  10                  15



(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:      187:

        (i)  SEQUENCE CHARACTERISTICS:

                (A)  LENGTH:                 16
                (B)  TYPE:                   amino acid
                (C)  STRANDEDNESS:
                (D)  TOPOLOGY:               linear

        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys
                     5                  10                  15
```

(2) INFORMATION FOR SEQ ID NO:188:

      (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 151 amino acids
       (B) TYPE: amino acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: peptide

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

```
Cys Thr Ala Cys Ala Thr Cys Thr Ala Cys Ala Thr Cys Cys Ala Cys
1               5                   10                  15
Cys Ala Cys Thr Gly Gly Gly Ala Cys Ala Ala Gly Cys Cys Ala Thr
                20                  25                  30
Cys Thr Thr Gly Thr Ala Ala Ala Ala Thr Gly Thr Gly Cys Gly Gly
        35                  40                  45
Ala Gly Ala Ala Gly Gly Ala Gly Ala Ala Ala Ala Cys Thr Thr Thr
    50                  55                  60
Cys Thr Gly Thr Gly Thr Gly Ala Ala Thr Gly Gly Ala Gly Gly Gly
65              70                  75                  80
Gly Ala Gly Thr Gly Cys Thr Thr Cys Ala Thr Gly Gly Thr Gly Ala
                85                  90                  95
Ala Ala Gly Ala Cys Cys Thr Thr Thr Cys Ala Ala Ala Cys Cys Cys
            100                 105                 110
Cys Thr Cys Gly Ala Gly Ala Thr Ala Cys Thr Thr Gly Thr Gly Cys
        115                 120                 125
Thr Cys Gly Gly Gly Cys Thr Cys Cys Ala Thr Gly Ala Ala Gly Ala
    130                 135                 140
Ala Gly Ala Thr Gly Thr Ala
145                 150
```

(2) INFORMATION FOR SEQ ID NO:189:

      (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 211 amino acids
       (B) TYPE: amino acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: peptide

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

```
Cys Thr Ala Cys Ala Thr Cys Thr Ala Cys Ala Thr Cys Cys Ala Cys
1               5                   10                  15
Cys Ala Cys Thr Gly Gly Gly Ala Cys Ala Ala Gly Cys Cys Ala Thr
                20                  25                  30
Cys Thr Thr Gly Thr Ala Ala Ala Ala Thr Gly Thr Gly Cys Gly Gly
```

```
              35                    40                   45
Ala Gly Ala Ala Gly Gly Ala Gly Ala Ala Ala Ala Cys Thr Thr Thr
    50                    55                   60
Cys Thr Gly Thr Gly Thr Gly Ala Ala Thr Gly Gly Ala Gly Gly Gly
65                    70                   75                   80
Gly Ala Gly Thr Gly Cys Thr Thr Cys Ala Thr Gly Gly Thr Gly Ala
                  85                    90                   95
Ala Ala Gly Ala Cys Cys Thr Thr Thr Cys Ala Ala Ala Cys Cys Cys
                  100                   105                  110
Cys Thr Cys Gly Ala Gly Ala Thr Ala Cys Thr Thr Gly Thr Gly Cys
                  115                   120                  125
Ala Ala Gly Thr Gly Cys Cys Cys Ala Ala Ala Thr Gly Ala Gly Thr
    130                   135                  140
Thr Thr Ala Cys Thr Gly Gly Thr Gly Ala Thr Cys Gly Cys Thr Gly
    145                   150                  155                  160
Cys Cys Ala Ala Ala Ala Cys Thr Ala Cys Gly Thr Ala Ala Thr Gly
                  165                   170                  175
Gly Cys Cys Ala Gly Cys Thr Thr Cys Thr Ala Cys Thr Cys Cys Ala
                  180                   185                  190
Thr Gly Ala Ala Gly Ala Ala Gly Ala Thr Gly Thr Ala Cys Cys Thr
                  195                   200                  205
Gly Cys Thr
    210
```

-193-